

# CRF Errors Corrected by the STIC Systems Branch

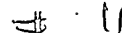
Serial Number: 09/943,075A

CRF Processing Date: 7/3/02  
 Edited by: DC  
 Verified by: \_\_\_\_\_ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: ENTERED
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95




OIEP

## RAW SEQUENCE LISTING

DATE: 07/03/2002

PATENT APPLICATION: US/09/943,075A

TIME: 13:57:31

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\07032002\I943075A.raw

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4 <110> APPLICANT: Popoff, Steven N.
5   Safado, Favez F.
6   Owen, Thomas A.
7   Smock, Steven L.
9 <120> TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
10  Compositions and Methods of Stimulating Bone Differentiation
12 <130> FILE REFERENCE: 71369.262
14 <140> CURRENT APPLICATION NUMBER: US 09/943,075A
15 <141> CURRENT FILING DATE: 2001-08-30
17 <150> PRIOR APPLICATION NUMBER: US 60/229,006
18 <151> PRIOR FILING DATE: 2000-08-30
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2320
26 <212> TYPE: DNA
27 <213> ORGANISM: Rat osteoactivin
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (115)...(1833)
33 <400> SEQUENCE: 1
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35 ctaggagatc agagtcaagc cctgactggc tgagggcgagg cgctccgagt cagc atg 117
36                                     Met
37                                     1
39 gaa agt ctc tgc ggg gtc ctg gta ttt ctg ctg ctg gct gca gga ctg 165
40 Glu Ser Leu Cys Gly Val Leu Val Phe Leu Leu Leu Ala Ala Gly Leu
41      5                      10                      15
43 ccg ctc cag gcg gcc aag cgg ttc cgt gat gtg ctg ggc cat gag cag 213
44 Pro Leu Gln Ala Ala Lys Arg Phe Arg Asp Val Leu Gly His Glu Gln
45      20                      25                      30
47 tat ccg gat cac atg agg gag aac aac caa tta cgt ggc tgg tct tca 261
48 Tyr Pro Asp His Met Arg Glu Asn Asn Gln Leu Arg Gly Trp Ser Ser
49      35                      40                      45
51 gat gaa aat gaa tgg gat gaa cag ctg tat cca gtg tgg agg agg gga 309
52 Asp Glu Asn Glu Trp Asp Glu Gln Leu Tyr Pro Val Trp Arg Arg Gly
53      50                      55                      60                      65
55 gag ggc aga tgg aag gac tcc tgg gaa gga ggc cgt gtg cag gca gcc 357
56 Glu Gly Arg Trp Lys Asp Ser Trp Glu Gly Gly Arg Val Gln Ala Ala
57      70                      75                      80
59 cta acc agt gat tca ccg gcc ttg gtg ggt tcc aat atc acc ttc gta 405
60 Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe Val
61      85                      90                      95

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63 gtg aac ctg gtg ttc ccc aga tgc cag aag gaa gat gcc aac ggc aat 453
64 Val Asn Leu Val Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly Asn
65      100      105      110
67 atc gtc tat gag agg aac tgc aga agt gat ttg gag ctg gct tct gac 501
68 Ile Val Tyr Glu Arg Asn Cys Arg Ser Asp Leu Glu Leu Ala Ser Asp
69      115      120      125
71 ccg tat gtc tac aac tgg acc aca ggg gca gac gat gag gac tgg gaa 549
72 Pro Tyr Val Tyr Asn Trp Thr Thr Gly Ala Asp Asp Glu Asp Trp Glu
73 130      135      140      145
75 gac aac acc agc caa ggc cag cac ctc agg ttc ccc gac ggg aag ccc 597
76 Asp Asn Thr Ser Gln Gly Gln His Leu Arg Phe Pro Asp Gly Lys Pro
77      150      155      160
79 ttc cct cgc ccc cac gga cgg aag aaa tgg aac ttc gtc tac gtc ttc 645
80 Phe Pro Arg Pro His Gly Arg Lys Lys Trp Asn Phe Val Tyr Val Phe
81      165      170      175
83 cac aca ctt ggt cag tat ttt caa aag ctg ggt cag tgt tca gca cga 693
84 His Thr Leu Gly Gln Tyr Phe Gln Lys Leu Gly Gln Cys Ser Ala Arg
85      180      185      190
87 gtt tct ata aac aca gtc aac ttg aca gtt ggc cct cag gtc atg gaa 741
88 Val Ser Ile Asn Thr Val Asn Leu Thr Val Gly Pro Gln Val Met Glu
89      195      200      205
91 gtg att gtc ttt cga aga cac ggc cgg gca tac att ccc atc tcc aaa 789
92 Val Ile Val Phe Arg Arg His Gly Arg Ala Tyr Ile Pro Ile Ser Lys
93 210      215      220      225
95 gtg aaa gac gtg tat gtg ata aca gat cag atc cct ata ttc gtg acc 837
96 Val Lys Asp Val Tyr Val Ile Thr Asp Gln Ile Pro Ile Phe Val Thr
97      230      235      240
99 atg tac cag aag aat gac cgg aac tcg tct gat gaa acc ttc ctc aga 885
100 Met Tyr Gln Lys Asn Asp Arg Asn Ser Ser Asp Glu Thr Phe Leu Arg
101      245      250      255
103 gac ctc ccc att ttc ttc gat gtc ctc att cac gat ccc agt cat ttc 933
104 Asp Leu Pro Ile Phe Phe Asp Val Leu Ile His Asp Pro Ser His Phe
105      260      265      270
107 ctc aac tac tct gcc att tcc tac aag tgg aac ttt ggg gac aac act 981
108 Leu Asn Tyr Ser Ala Ile Ser Tyr Lys Trp Asn Phe Gly Asp Asn Thr
109      275      280      285
111 ggc ctg ttt gtc tcc aac aat cac act ttg aat cac acg tat gtg ctc 1029
112 Gly Leu Phe Val Ser Asn Asn His Thr Leu Asn His Thr Tyr Val Leu
113 290      295      300      305
115 aat gga acc ttc aac ttt aac ctc acc gtg caa act gca gtg ccg gga 1077
116 Asn Gly Thr Phe Asn Phe Asn Leu Thr Val Gln Thr Ala Val Pro Gly
117      310      315      320
119 cca tgc ccc tca ccc aca cct tcg cct tct tct tcg act tct cct tcg 1125
120 Pro Cys Pro Ser Pro Thr Pro Ser Pro Ser Ser Ser Thr Ser Pro Ser
121      325      330      335
123 cct gca tct tcg cct tca ccc aca tta tca aca cct agt ccc tct tta 1173
124 Pro Ala Ser Ser Pro Ser Pro Thr Leu Ser Thr Pro Ser Pro Ser Leu
125      340      345      350
127 atg cct act ggc tac aaa tcc atg gag ctg agt gac att tcc aat gaa 1221

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128 Met Pro Thr Gly Tyr Lys Ser Met Glu Leu Ser Asp Ile Ser Asn Glu
129      355      360      365
131 aac tgc cga ata aac aga tat ggt tac ttc aga gcc acc atc aca att 1269
132 Asn Cys Arg Ile Asn Arg Tyr Gly Tyr Phe Arg Ala Thr Ile Thr Ile
133 370      375      380      385
135 gta gat gga atc cta gaa gtc aac atc atc cag gta gca gat gtc cca 1317
136 Val Asp Gly Ile Leu Glu Val Asn Ile Ile Gln Val Ala Asp Val Pro
137      390      395      400
139 atc ccc aca ctg cag cct gac aac tca ctg atg gac ttc att gtg acc 1365
140 Ile Pro Thr Leu Gln Pro Asp Asn Ser Leu Met Asp Phe Ile Val Thr
141      405      410      415
143 tgc aaa ggg gcc act ccc acg gaa gcc tgt acg atc atc tct gac ccc 1413
144 Cys Lys Gly Ala Thr Pro Thr Glu Ala Cys Thr Ile Ile Ser Asp Pro
145      420      425      430
147 acc tgc cag atc gcc cag aac agg gtg tgc agc ccg gtg gct gtg gat 1461
148 Thr Cys Gln Ile Ala Gln Asn Arg Val Cys Ser Pro Val Ala Val Asp
149      435      440      445
151 gag ctg tgc ctc ctg tcc gtg agg aga gcc ttc aat ggg tcc ggc acg 1509
152 Glu Leu Cys Leu Leu Ser Val Arg Arg Ala Phe Asn Gly Ser Gly Thr
153 450      455      460      465
155 tac tgt gtg aat ttc act ctg gga gac gat gca agc ctg gcc ctc acc 1557
156 Tyr Cys Val Asn Phe Thr Leu Gly Asp Asp Ala Ser Leu Ala Leu Thr
157      470      475      480
159 agc gcc ctg atc tct atc cct ggc aaa gac cta ggc tcc cct ctg aga 1605
160 Ser Ala Leu Ile Ser Ile Pro Gly Lys Asp Leu Gly Ser Pro Leu Arg
161      485      490      495
163 aca gtg aat ggt gtc ctg atc tcc att ggc tgc ctg gcc atg ttt gtc 1653
164 Thr Val Asn Gly Val Leu Ile Ser Ile Gly Cys Leu Ala Met Phe Val
165      500      505      510
167 acc atg gtt acc atc ttg ctg tac aaa aaa cac aag acg tac aag cca 1701
168 Thr Met Val Thr Ile Leu Leu Tyr Lys Lys His Lys Thr Tyr Lys Pro
169      515      520      525
171 ata gga aac tgc acc agg aac gtg gtc aag ggc aaa ggc ctg agt gtt 1749
172 Ile Gly Asn Cys Thr Arg Asn Val Val Lys Gly Lys Gly Leu Ser Val
173 530      535      540      545
175 ttt ctc agc cat gca aaa gcc ccg ttc tcc cga gga gac cgg gag aag 1797
176 Phe Leu Ser His Ala Lys Ala Pro Phe Ser Arg Gly Asp Arg Glu Lys
177      550      555      560
179 gat cca ctg ctc cag gac aag cca tgg atg ctc taa gtcttcactc 1843
180 Asp Pro Leu Leu Gln Asp Lys Pro Trp Met Leu *
181      565      570
183 tcacttctga ctgggaaccc actcttctgt gcatgtatgt gagctgtgca gaagtacatg 1903
184 actggtagct gttgttttct acgattatt gtaaatgta tatcatggtt tagggagtgt 1963
185 agttaattgg catttttagtg aagggatggg aagacagtat ttcttcgcat ctgtattgtg 2023
186 gttttatata tgtaatatgg gtgggcacat tgtgtctgaa gggggagggg gaggtcactg 2083
187 ctacttaagg tcttaggtta actgggagag gatgccccag gctccttaga ttctacaca 2143
188 agatgtgocg gaacccagct agtcttgacc taaaggccat gcttcatcaa ctctatctca 2203
189 gctcattgaa catacctgag cgctgatgg aattataatg gaaccaagct tgttgtatgg 2263
190 tgtgtgtgtg tacataagat actcattaaa aagacagtct attaaaaaaa aaaaaaa 2320

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192 <210> SEQ ID NO: 2
193 <211> LENGTH: 572
194 <212> TYPE: PRT
195 <213> ORGANISM: Rat osteoactivin
197 <400> SEQUENCE: 2
198 Met Glu Ser Leu Cys Gly Val Leu Val Phe Leu Leu Leu Ala Ala Gly
199 1 5 10 15
200 Leu Pro Leu Gln Ala Ala Lys Arg Phe Arg Asp Val Leu Gly His Glu
201 20 25 30
202 Gln Tyr Pro Asp His Met Arg Glu Asn Asn Gln Leu Arg Gly Trp Ser
203 35 40 45
204 Ser Asp Glu Asn Glu Trp Asp Glu Gln Leu Tyr Pro Val Trp Arg Arg
205 50 55 60
206 Gly Glu Gly Arg Trp Lys Asp Ser Trp Glu Gly Gly Arg Val Gln Ala
207 65 70 75 80
208 Ala Leu Thr Ser Asp Ser Pro Ala Leu Val Gly Ser Asn Ile Thr Phe
209 85 90 95
210 Val Val Asn Leu Val Phe Pro Arg Cys Gln Lys Glu Asp Ala Asn Gly
211 100 105 110
212 Asn Ile Val Tyr Glu Arg Asn Cys Arg Ser Asp Leu Glu Leu Ala Ser
213 115 120 125
214 Asp Pro Tyr Val Tyr Asn Trp Thr Thr Gly Ala Asp Asp Glu Asp Trp
215 130 135 140
216 Glu Asp Asn Thr Ser Gln Gly Gln His Leu Arg Phe Pro Asp Gly Lys
217 145 150 155 160
218 Pro Phe Pro Arg Pro His Gly Arg Lys Lys Trp Asn Phe Val Tyr Val
219 165 170 175
220 Phe His Thr Leu Gly Gln Tyr Phe Gln Lys Leu Gly Gln Cys Ser Ala
221 180 185 190
222 Arg Val Ser Ile Asn Thr Val Asn Leu Thr Val Gly Pro Gln Val Met
223 195 200 205
224 Glu Val Ile Val Phe Arg Arg His Gly Arg Ala Tyr Ile Pro Ile Ser
225 210 215 220
226 Lys Val Lys Asp Val Tyr Val Ile Thr Asp Gln Ile Pro Ile Phe Val
227 225 230 235 240
228 Thr Met Tyr Gln Lys Asn Asp Arg Asn Ser Ser Asp Glu Thr Phe Leu
229 245 250 255
230 Arg Asp Leu Pro Ile Phe Phe Asp Val Leu Ile His Asp Pro Ser His
231 260 265 270
232 Phe Leu Asn Tyr Ser Ala Ile Ser Tyr Lys Trp Asn Phe Gly Asp Asn
233 275 280 285
234 Thr Gly Leu Phe Val Ser Asn Asn His Thr Leu Asn His Thr Tyr Val
235 290 295 300
236 Leu Asn Gly Thr Phe Asn Phe Asn Leu Thr Val Gln Thr Ala Val Pro
237 305 310 315 320
238 Gly Pro Cys Pro Ser Pro Thr Pro Ser Pro Ser Ser Thr Ser Pro
239 325 330 335
240 Ser Pro Ala Ser Ser Pro Ser Pro Thr Leu Ser Thr Pro Ser Pro Ser
241 340 345 350

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242 Leu Met Pro Thr Gly Tyr Lys Ser Met Glu Leu Ser Asp Ile Ser Asn
243           355           360           365
244 Glu Asn Cys Arg Ile Asn Arg Tyr Gly Tyr Phe Arg Ala Thr Ile Thr
245           370           375           380
246 Ile Val Asp Gly Ile Leu Glu Val Asn Ile Ile Gln Val Ala Asp Val
247 385           390           395           400
248 Pro Ile Pro Thr Leu Gln Pro Asp Asn Ser Leu Met Asp Phe Ile Val
249           405           410           415
250 Thr Cys Lys Gly Ala Thr Pro Thr Glu Ala Cys Thr Ile Ile Ser Asp
251           420           425           430
252 Pro Thr Cys Gln Ile Ala Gln Asn Arg Val Cys Ser Pro Val Ala Val
253           435           440           445
254 Asp Glu Leu Cys Leu Leu Ser Val Arg Arg Ala Phe Asn Gly Ser Gly
255           450           455           460
256 Thr Tyr Cys Val Asn Phe Thr Leu Gly Asp Asp Ala Ser Leu Ala Leu
257 465           470           475           480
258 Thr Ser Ala Leu Ile Ser Ile Pro Gly Lys Asp Leu Gly Ser Pro Leu
259           485           490           495
260 Arg Thr Val Asn Gly Val Leu Ile Ser Ile Gly Cys Leu Ala Met Phe
261           500           505           510
262 Val Thr Met Val Thr Ile Leu Leu Tyr Lys Lys His Lys Thr Tyr Lys
263           515           520           525
264 Pro Ile Gly Asn Cys Thr Arg Asn Val Val Lys Gly Lys Gly Leu Ser
265           530           535           540
266 Val Phe Leu Ser His Ala Lys Ala Pro Phe Ser Arg Gly Asp Arg Glu
267 545           550           555           560
268 Lys Asp Pro Leu Leu Gln Asp Lys Pro Trp Met Leu
269           565           570
272 <210> SEQ ID NO: 3
273 <211> LENGTH: 18
274 <212> TYPE: PRT
275 <213> ORGANISM: Rat osteoactivin
277 <400> SEQUENCE: 3
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279 1           5           10           15
280 Asp Glu
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 19
286 <212> TYPE: PRT
287 <213> ORGANISM: Rat osteoactivin
289 <400> SEQUENCE: 4
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291 1           5           10           15
292 Asp Lys Cys
296 <210> SEQ ID NO: 5
297 <211> LENGTH: 574
298 <212> TYPE: PRT
299 <213> ORGANISM: Mouse
301 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

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